

Cyr61	M--SSSTFRLAVAVTLIHL--TRIALST-CPAAC--HGFLE-APKCAPGVGLVLDGQGGYKQK	58
CEP10	M--GSAGARP-ALAAAILCL--ARLALGSPCPAVC--QGFAP-ABQCAPGVGLVLDGQGGYKQK	58
Fisp12	M--LASVAGTISLA-LVLLALCTRPATGQDCSAQC--QCAAEAPNCPAGVSLVLDGQGGYKQK	61
CTGF	M--TAASHGTVRVAFVVLALCSPAVGQNCSCPC--RCTDEPAPNCPAGVSLVLDGQGGYKQK	62
Nov	METGCGQGLFVLLIIIIITLRFCEVSGREAACPRPGGRCPAEP-PRCAPGVFAVLDGQGGYKQK	65
Cyr61	QLNEDCSKTQPCDHKXGLECNFGASSTALNGICRAQSEGRPCFYNSKIYONGESTQPNCHQCTCI	124
CEP10	QLNEDCSKTQPCDHKXGLECNFGASPAATNGICRAQSEGRPCFYNSKIYONGESTQPNCHQCTCI	124
Fisp12	QLGZLCTERDECDPHKGLFCDFGSPANRKIGVCTAK-DGAPCVFGSVYRSSESISSEKYNQCTCI	126
CTGF	QLGZLCTERDECDPHKGLFCDFGSPANRKIGVCTAK-DGAPCVFGSVYRSSESISSEKYNQCTCI	127
Nov	RRGZSCSPILPCDESGETYCDRGPEDCGGAGICMVL-EGDNQVFDGKIDRNGETEDPSIKYDCTCI	130
Cyr61	DGAVGCTFLCPQELSLFNLCGPNFRLVKVSGCCGEWVCDSDSIK-DSLDD-QDDLLGLDASEVEL	188
CEP10	DGAVGCTFLCPQELSLFNLCGPNFRLVKVSGCCGEWVCDSDSDALEELEGFFSKFGLDASEVEL	190
Fisp12	DGAVGCTFLCSHVRFLSPDCPFPRRVKLPCKCKGEWVCDPEKDKTAVGP-----ALAKYRLSD	185
CTGF	DGAVGCTFLCSHVRFLSPDCPFPRRVKLPCKCKGEWVCDPEKDKTAVGP-----ALAKYRLSD	186
Nov	DGQIGGLPRCHLGLLLPCPDGPFPRKI EVPGCECKVWCDPRDEVLLCGF-----ANAKYRQEA	189
Cyr61	TRNNELIAIGKSSSLQKLPVFCUTEFVLFNPLHAGQKCTVQTTSSSQCSKSGGTGLSTKVTNDMP	254
CEP10	TRNNELIAIVKGG-LQKLPVFCSEFQ-----SRAFENPKGIVQTTSSSQCSKSGGTGLSTKVTNDMP	251
Fisp12	T-----FGPDF-----THIRANGLVQTTSSSACSSTCGGTGLSTKVTNDMP	225
CTGF	T-----FGPDF-----THIRANGLVQTTSSSACSSTCGGTGLSTKVTNDMP	226
Nov	T-----LGIDV-----SDSSANGTEQTTSSSACSSTCGGTGLSTKVTNDMP	229
Cyr61	ECRLVKETRIEVRPCGQPVYSSLIQKQKCKKCKPSPEVRFYAGCSSVQCYRPKYCGSVDGRC	320
CEP10	DCKLIKETRIEVRPCGQPSYASLIQKQKCKKCKPSPEVRFYAGCSSVQCYRPKYCGSVDGRC	317
Fisp12	FCRLKQSELEHVRPEADLEENIQKQKCKKCKKIPCLAKPVKFLSGGTSVQCYRAKFGGVTGGRG	291
CTGF	SCRLEKQSELEHVRPEADLEENIQKQKCKKCKKIPCLAKPVKFLSGGTSVQCYRAKFGGVTGGRG	292
Nov	QCEVKEQTELEHVRPCEN-EEPSDKQKCKKCTQDKSHKAVFEXNGTSSVQCYRKYCGLENDGRG	294
Cyr61	CTPLOTRTVQKFRFCEDGGEFTSIVVM-IQSCRCNYNCPHREASTRLY--SLFNDIHKFRD	379
CEP10	CTPQOTRTVQKFRFCDDGETFTKSVM-IQSCRCNYNCPHANEY-YFFY--RLVNDIHKFRD	376
Fisp12	CTPHRTITLTVFVKCPDGEVMOON-HMFIKTCACHYNCPCDNDIFESLYRYMYGDMA	348
CTGF	CTPHRTITLTVFVKCPDGEVMOON-HMFIKTCACHYNCPCDNDIFESLYRYMYGDMA	349
Nov	CTPHNDKTIQVEFRCPQGGFLKKP-HMLNTGVCHGNCPCQSKNAFTQPLDPMSEAKI	351

FIGURE 1

M--SSSTFRTLAVAVTLLHL--TRLALST-CPAAC--HCPL-APKCAPGVGLVRDGGCGCKVCAK
 M--GSAGARP-ALAAALLCL--ARLALGSPCAVC--QCPAA-APQCAPGVGLVPDGGCGCKVCAK
 M--LASVAGPISLA-LVLLALCTRPATGQDCSAQC--OCAAEEAAPHCPAGVSLVLDGGCGCCRCAK
 M--TAASMGVVRVAFVLLALCSRPAVGQNCSGPC--RCPDEPAPRPCAGVSLVLDGGCGCCRCAK
 METGGGQGLPVLLLLLLLRPCEVSGREAAACPRPCGGRCPAEP-PRCAPGVPAVLDGGCGCCLVCAR

Cyr61
 CEF10
 FISP12
 CTGF
 Nov

QLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCYNSRIYONGESFOPNCKHQCTCI
 QLNEDCSRTQPCDHTKGLECNFGASPAATNGICRAQSEGRPCYNSKIYONGESFOPNCKHQCTCI
 QLGELCTERDPCDPHKGLFCDFGSPANRKIGVCTAK-DGAPCVFGGSVYRSGESFOSCKYQCTCL
 QLGELCTERDPCDPHKGLFCDFGSPANRKIGVCTAK-DGAPCIFGGTVYRSGESFOSCKYQCTCL
 ORGESCSPLLPDESGLYCDRGPEDGGGAGICMVL-EGDNCVFDGMIYRNGETFOPSCKYQCTCR

Cyr61
 CEF10
 FISP12
 CTGF
 Nov

DGAVGCIPLCPOELSLPNLGCNPRLVKVSGQCCEEWVCEDESIK-DSLDD-ODDLLGLDASEVEL
 DGAVGCIPLCPOELSLPNLGCPSRPLVKVPGQCCEEWVCEDESKDALEELEGFFSKEFGLDASEGEL
 DGAVGCVPLCSMDVRLSPDCPFPRRVKLPKGCKCKEWVCEDEPKDRTAVGP-----ALAAAYRLED
 DGAVGCMPLCSMDVRLSPDCPFPRRVKLPKGCKCEEWVCEDEPKDQTVVGP-----ALAAAYRLED
 DGQIGCLPRCNLGLLLPGPDCPFPRKIEVPGECKEWVCDPRDEVLLGGF-----AMAAAYRQEA

Cyr61
 CEF10
 FISP12
 CTGF
 Nov

FIGURE 1 (1 of 2)

Cyr61	TRNNELIAIGKSSLRPLPVFGTEPRVLFNPLHAHGOKCIVQTTWSQCSKSGTGISTRVTNDNP	254
CEF10	TRNNELIAIVKGG-LKMLPVFGSEPQ-----SRAFENPKCIVQTTWSQCSKTCGTGISTRVTNDNP	251
Fisp12	T-----FGPDP-----TMMRANCLVQTTESACSKTCGMGISTRVTNDNT	225
CTGF	T-----FGPDP-----TMIRANCLVQTTESACSKTCGMGISTRVTNDNA	226
Nov	T-----LGIDV-----SDSSANCIEQTTESACSKSCGMGFSTRVTRNRNQ	229

Cyr61	ECRLVKETRICEVRPCGQPVYSSLKGGKKCKTKKSPPEVRFTYAGCSSVKKYRPKYCGSCVDGRC	320
CEF10	DCKLIKETRICEVRPCGQPSYASLKGKKCTKTKKSPSPVRFTYAGCSSVKKYRPKYCGSCVDGRC	317
Fisp12	FCRLEKOSRLCMVRPCEADLEENIKGKKCIRTPIAKPVKFELSGCTSVKTYRAKFCGVCTDGRC	291
CTGF	SCRLEKOSRLCMVRPCEADLEENIKGKKCIRTPIKSKPIKFELSGCTSMKTYRAKFCGVCTDGRC	292
Nov	QCEMVKQTRLCMMRPCEN-EEPSDKGKKCIOTKSKMAVRFEYKNCTSVQTYKPRYCGLCNDGRC	294

Cyr61	CTPLQTRTVKMRFCEDGEMFSKNVMM-IQSCKCNYNCPHPNEASFRLY--SLFNDIHKFRD	379
CEF10	CTPQQTRTVKIRFRCDGGETFTKSVM-MQSCRCNYNCPHANEAFYFY--RLVNDIHKFRD	376
Fisp12	CTPHRTTTLPVEFKCPDGEIMKKN-MMFIKTCACHYNCPGDNDIFESLYRKMVGDMA	348
CTGF	CTPHRTTTLPVEFKCPDGEVMKKN-MMFIKTCACHYNCPGDNDIFESLYRKMVGDMA	349
Nov	CTPHNTKTIQVEFRCPQKFLKPP-MMLINTCVCHGNCPOSNAFFQPLDPMSEAKI	351

FIGURE 1 (2 of 2)